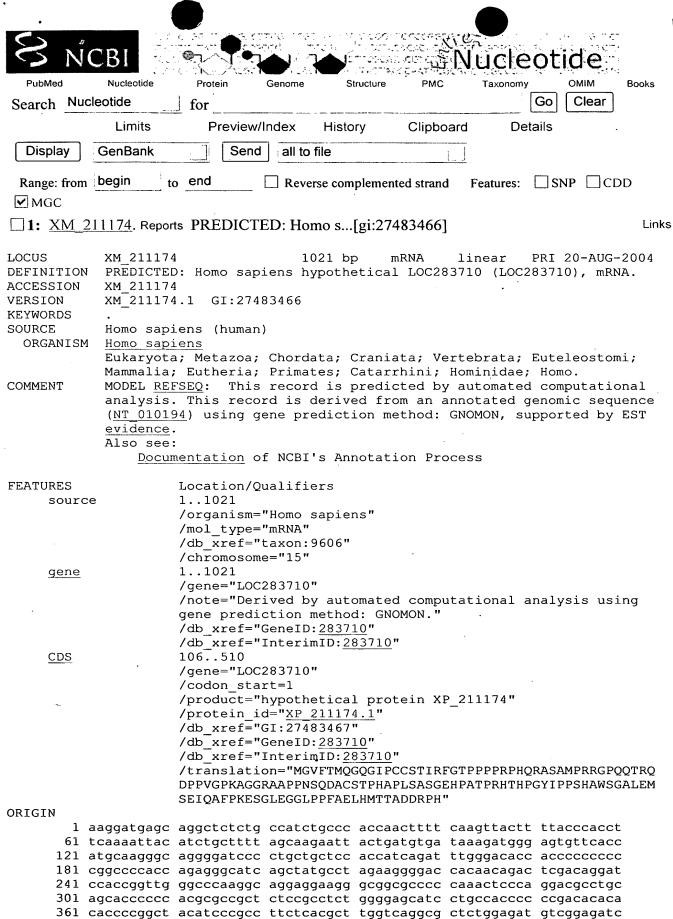
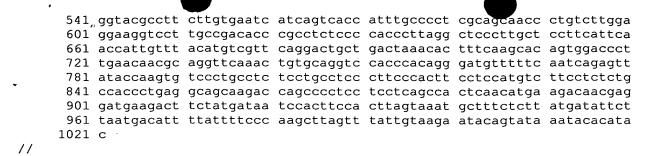
10

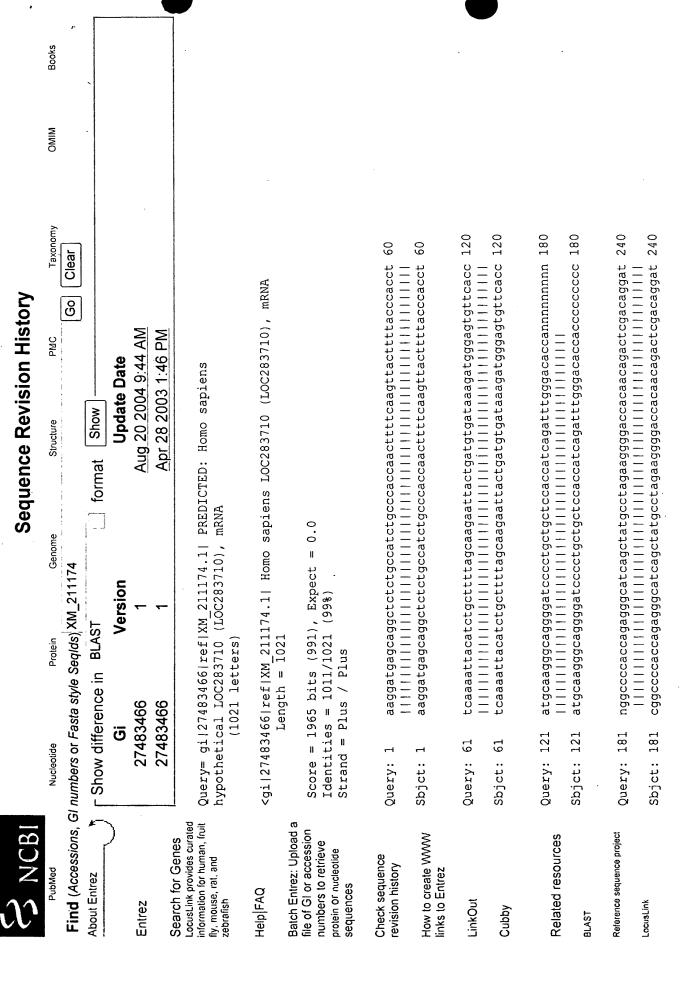


421 caggetttte etaaagagte aggattggaa ggeggaetee eacegtttge tgageteeae 481 atgacaacag cagaegaeag geegeaetga teecaeetgg ettaeaggtg etgteaeaca



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Dec 16 2004 18:01:17



Clusters of orthologous groups	Query:	241	ccaccggttgggcccaaggcaggaaggaaggcgcqcccccaaactcccaggacgcctgc 300
Protein reviews on the web		241	
	Query: Sbjct:	301	agcacccccacgcgccgctctccgcctctggggagcatcctgccacccccgacacaca 360
	Query: Sbjct:	361 361	caccccggctacatcccgccttctcacgcttggtcaggcgctctggagatgtcggagatc 420
	Query: Sbjct:	421	caggettttectaaagagteaggattggaaggeggaeteceaeegtttgetgagetecae 480
	Query: Sbjct:	481	atgacaacagcagacgacaggccgcactgatcccacctggcttacaggtgctgtcacaca 540
	Query: Sbjct:	541 541	
	Query: Sbjct:	601	ggaaggteettgeegacacegeeteteeceacettaggeteeettgeteetteattea 660
	Query: (Sbjct: (661	accattgtttacatgtcgttcaggactgctgactaaacactttcaagcacagtggaccct 720

2004/12/24

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taatgacattttattttcccaagcttagtttattgtaagaatacagtataaatacacata 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             taatgacattttattttcccaagcttagtttattgtaagaatacagtataaatacacata 1020
 780
                                                   780
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                                                                                                                                                                                                                                                                                                              ccaccetgaggcagcaagaccagccettectecteagccactcaacatgaagacaacgag 900
                                                                                                                                                                                                                                                                                                                                                                                                                                               960
                                                   tgaacaacgcaggttcaaactgtgcaggtccacccacagggatgttttcaatcagagtt
   tgaacaacgcaggttcaaactgtgcaggtccaccacagggatgttttcaatcagagtt
                                                                                                                                                                                ataccaagtgtccctgcctcctgcctcccttcccacttcctccatgtcttcctctctg
                                                                                                                                                                                                                                                           ccaccctgaggcagcaagaccagcccttctctcagccactcaacatgaagacaacgag
                                                                                                                                                                                                                                                                                                                                                                                            gatgaagacttctatgataatccacttccacttagtaaatgctttctcttatgatattct
                                                                                                                                                                                                                                                                                                                                                                                                                                               gatgaagacttctatgataatccacttccacttagtaaatgctttctcttatgatattct
                                                                                                                                ataccaagtgtccctgcctctcctgcctcccttcccacttcctccatgtcttcctctctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score = 32.2 bits (16), Expect = 2e-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sbjct: 144 gcaggggatccctgc 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query: 129 gcaggggatccctgc 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identities = 16/16 (100%)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strand = Plus / Minus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query: 1021 c 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sbjct: 1021
Query: 721
                                                 Sbjct: 721
                                                                                                                             Query: 781
                                                                                                                                                                                                                                                          Query: 841
                                                                                                                                                                                                                                                                                                             Sbjct: 841
                                                                                                                                                                                                                                                                                                                                                                                          Query: 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query: 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sbjct: 961
                                                                                                                                                                                Sbjct: 781
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sbjct: 901
```

工

 \times

Lambda

```
1.31
0.711
1.37
```

0.711 Lambda Gapped

1.31

Gap Penalties: Existence: 5, Extension: 2 Matrix: blastn matrix:1 -3

Number of Hits to DB: 3

Number of Sequences: 0

Number of extensions: 3

Number of successful extensions: 3

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

0 Number of HSP's successfully gapped in prelim test: 0 Number of HSP's that attempted gapping in prelim test:

Number of HSP's gapped (non-prelim): 3

length of query: 1021

length of database: 1021

effective HSP length: 9

effective length of query: 1012

effective length of database: 1012 effective search space: 1024144

effective search space used: 1024144

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 9 (18.3 bits)

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$\mathcal{X}^{ ext{RGB}}$			Sed	Sequence Revision History	vision	History			
Рирмед	Nucleotide	Protein	Genome	Structure		PMC	Taxonomy	OMIM	Books
Find (Accessions, G	Find (Accessions, GI numbers or Fasta style SeqIds) XM_211174	Seqids) XM_211	174	and supplications or one on the supplication of the supplication o	and the second party of the second desired and the second	ගි	Clear		
About Entrez	F Show difference in GenBank/GenPept Diff	GenBank/Ger	t Diff	format Show	[M		ARTHUR		
)	ច	Version	_	Upo	Update Date				
Entrez	27483466	_		Aug 20 2	Aug 20 2004 9:44 AM	AM		•	
Social forces	27483466	A CONTRACTOR OF THE PROPERTY O	***************************************	Apr 28 2	Apr 28 2003 1:46 PM	PM			
Search to Gerres LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish	Accession = XM_211174, L	ocus =====	= XM_211174 ==================================				·		
Help FAQ	Differences in LOCUS nam	SUS names:							
Batch Entrez: Upload a file of GI or accession	old: "LOCUS 28-APR-2003"	XM_211174		1021 bp	mRNA	linear	PRI		
numbers to retrieve protein or nucleotide sequences	new: "LOCUS 20-AUG-2004"	XM_211174		1021 bp	mRNA	linear	PRI		
Check sequence revision history	Differences in DEFINITION:	TINITION:		٠					
How to create WWW	old: "Homo sapiens LOC283710	s LOC283710	(LOC283710), mRNA."	mRNA."					
links to Entrez LinkOut	new: "PREDICTED: Homo sapiens hypothetical LOC283710	lomo sapiens	hypothetica	1 LOC283710	(LOC283	(LOC283710), mRNA."	A."		
Cubby	Differences in REFERENCE	FERENCE:							
	Old reference: refline:	"1 ()	(bases 1 to 1	1021)"					
Related resources	authors:	"Inte	"International Human		Sequenci	Genome Sequencing Consortium."	tium."		
BLAST	title: journal:	ndun	"Ine DNA sequence or "Unpublished (2003)"		nomo sapiens.	•			
Reference sequence project	Differences in COMMENT:	1MENT:							
LocusLink	old: "MODEL REFSEQ:	 This	record is predi	predicted by automated computational	comated c	omputatio	nal		

Clusters of orthologous groups

analysis. This record is derived from an annotated genomic sequence (NT_010194) using gene prediction method: BLAST, supported by EST

Protein reviews on the web

analysis. This record is derived from an annotated genomic sequence "MODEL REFSEQ: This record is predicted by automated computational (NT_010194) using gene prediction method: GNOMON, supported by EST evidence. Also see: Documentation of NCBI's Annotation Process " new:

evidence. Also see: Documentation of NCBI's Annotation Process "

Differences in FEATURE.CDS:

106..510 Changed feature CDS

= "GeneID:283710" /db_xref New

Differences in FEATURE.gene:

1..1021 Changed feature gene /db_xref /note New

analysis using gene prediction method: GNOMON." "Derived by automated computational = "GeneID:283710"

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